

U.S.S.N. 09/663,968

Yip

AMENDMENT

removing the residual baseline from the intermediate data set to generate a corrected data set;

locating a probable peak in the corrected data set; and

identifying, using the located probable peak, the biological sample.

12. (2x Amended) The method according to claim 11, wherein the threshold factor is selected so that higher stages of data are filtered less than lower stages.

13. (2x Amended) The method according to claim 5, further including generating a sparse data set comprising the denoised data.

19. (2x Amended) The method according to claim 1, further including the step of compressing the intermediate data set subsequent to removing the residual baseline, comprising

- a) generating an x-y array of coefficients from the intermediate data set;
- b) determining a data starting point and a data maximum;
- c) generating intermediate compressed data values for each data point; and
- d) calculating compressed data values to form a compressed data set; wherein the compressed data set is used in the locating step.

20. (2x Amended) The method according to claim 19, wherein the intermediate compressed data value is a real number that includes a whole number portion representing the non-zero wavelet coefficient of each of the denoised data.

21. (2x Amended) The method according to claim 19, wherein the intermediate compressed data value is a real number that includes a decimal portion representing the quotient of the value of the wavelet coefficient of the denoised data divided by the maximum wavelet coefficient value

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38. (2x Amended) A system for identifying a biological sample, the system comprising:

an instrument receiving the biological sample and generating a data set indicative of the composition of the biological sample;

a computer communicating to the instrument and configured to receive the generated data set, the computer performing the method of:

denoising the data set to generate denoised data;

correcting the baseline from the denoised data to generate an intermediate data set;

defining putative peaks for the biological sample;

using the putative peaks to remove residual baseline effects, generating a residual baseline;

removing the residual baseline from the intermediate data set to generate a corrected data set;

locating a probable peak in the corrected data set; and

identifying, using the located probable peak, the biological sample.

40. (Amended) A machine readable program operating on a computing device, the computing device being configured to receive a data set indicating composition of a biological sample, the program implement the steps of:

denoising the data set to generate denoised data;

correcting the baseline from the denoised data to generate an intermediate data set;

defining putative peaks for the biological sample;

using the putative peaks to remove residual baseline effects, generating a residual baseline;

removing the residual baseline from the intermediate data set to generate a corrected data set;

identifying, using the located probable peak, the biological sample.

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41. (Amended) A system for identifying a component of a DNA sample, comprising:

a mass spectrometer receiving the DNA sample and generating a data set indicative of the composition of the DNA sample;

a computing device configured to receive the data set, the computing device implementing the method comprising:

denoising the data set using wavelet transformation to generate denoised data;

correcting the baseline from the denoised data to generate a corrected data set, the corrected data set having putative peaks;

using the putative peaks to remove residual baseline effects;

locating a probable peak in the corrected data set; and

identifying, using the located probable peak, a component in the composition of the DNA sample.

42. (Amended) The system according to claim 41, where the method further includes using a statistical methodology to determine a probability that the located probable peak is an actual peak.

43. (Amended) The system according to claim 42, where the method further includes determining a confidence based on a the probability, wherein the method calls the component of the DNA sample when the confidence is sufficiently high; and

the method does not call the component when the confidence is not sufficiently high.

44. (Amended) The system according to claim 42, where the probability is about 100 percent.

45. (Amended) A system for identifying a component in a biological sample, comprising:

indicative of the component in the biological sample